RAW SEQUENCE LISTING   DATE: 07/17/2001
PATENT APPLICATION: US/09/715,035   TIME: 09:36:26

Input Set : A:\Mockel-5.ST25.txt
Output Set: N:\CRF3\07172001\I715035.raw   **ENTERED**

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 5 <110> APPLICANT: Mockel, Bettina
 7        Pfefferle, Walter
11 <120> TITLE OF INVENTION: Novel Nucleotide Sequences Encoding the pfkA Gene
15 <130> FILE REFERENCE: 21123/274441
19 <140> CURRENT APPLICATION NUMBER: 09/715,035
21 <141> CURRENT FILING DATE: 2000-11-20
25 <160> NUMBER OF SEQ ID NOS: 4
29 <170> SOFTWARE: PatentIn version 3.0
33 <210> SEQ ID NO: 1
35 <211> LENGTH: 1274
37 <212> TYPE: DNA
39 <213> ORGANISM: Corynebacterium glutamicum
43 <220> FEATURE:
45 <221> NAME/KEY: CDS
47 <222> LOCATION: (143)..(1171)
51 <400> SEQUENCE: 1
52 gtcgatttgt taatgaaact gcagctctgg cgattaaata agatggtcag agacagtttt      60
54 ttggcctgtc aacccctgtg attctcttat ttttgggtga ttgttccggc gcgggtgttg     120
56 tgatgggttt aatatggaag ac atg cga att gct act ctc acg tca ggc ggc     172
57                         Met Arg Ile Ala Thr Leu Thr Ser Gly Gly
58                          1               5                  10
60 gac tgc ccc gga cta aac gcc gtc atc cga gga atc gtc cgc aca gcc     220
61 Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala
62              15                  20                  25
64 agc aat gaa ttt ggc tcc acc gtc gtt ggt tat caa gac ggt tgg gaa     268
65 Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu
66              30                  35                  40
68 gga ctg tta ggc gat cgt cgc gta cag ctg tat gac gat gaa gat att     316
69 Gly Leu Leu Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile
70          45                  50                  55
72 gac cga atc ctc ctt cga ggc ggc acc att ttg ggc act ggt cgc ctc     364
73 Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu
74      60                  65                  70
76 cat ccg gac aag ttt aag gcc gga att gat cag att aag gcc aac tta     412
77 His Pro Asp Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu
78 75                  80                  85                  90
80 gaa gac gcc ggc atc gat gcc ctt atc cca atc ggt ggc gaa gga acc     460
81 Glu Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr
82              95                 100                 105
84 ctg aag ggt gcc aag tgg ctg tct gat aac ggt atc cct gtt gtc ggt     508
85 Leu Lys Gly Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly
86              110                 115                 120
88 gtc cca aag acc att gac aat gac gtg aat ggc act gac ttc acc ttc     556
89 Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe
90              125                 130                 135
92 ggt ttc gat act gct gtg gca gtg gct acc gac gct gtt gac cgc ctg     604
93 Gly Phe Asp Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu
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94      140                     145                     150
96 cac acc acc gct gaa tct cac aac cgt gtg atg atc gtg gag gtc atg        652
97 His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met
98 155                     160                     165                     170
100 ggc cgc cac gtg ggt tgg att gct ctg cac gca ggt atg gcc ggc ggt       700
101 Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly
102                     175                     180                     185
104 gct cac tac acc gtt att cca gaa gta cct ttc gat att gca gag atc       748
105 Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile
106                     190                     195                     200
108 tgc aag gcg atg gaa cgt cgc ttc cag atg ggc gag aag tac ggc att       796
109 Cys Lys Ala Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile
110             205                     210                     215
112 atc gtc gtt gcg gaa ggt gcg ttg cca cgc gaa ggc acc atg gag ctt       844
113 Ile Val Val Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu
114         220                     225                     230
116 cgt gaa ggc cac att gac cag ttc ggt cac aag acc ttc acg gga att       892
117 Arg Glu Gly His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile
118 235                     240                     245                     250
120 gga cag cag atc gct gat gag atc cac gtg cgc ctc ggc cac gat gtt       940
121 Gly Gln Gln Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val
122                     255                     260                     265
124 cgt acg acc gtt ctt ggc cac att caa cgt ggt gga acc cca act gct       988
125 Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala
126                     270                     275                     280
128 ttc gac cgt gtt ctg gcc act cgt tat ggt gtt cgt gca gct cgt gcg      1036
129 Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala
130             285                     290                     295
132 tgc cat gag gga agc ttt gac aag gtt gtt gct ttg aag ggt gag agc      1084
133 Cys His Glu Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser
134         300                     305                     310
136 att gag atg atc acc ttt gaa gaa gca gtc gga acc ttg aag gaa gtt      1132
137 Ile Glu Met Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val
138 315                     320                     325                     330
140 cca ttc gaa cgc tgg gtt act gcc cag gca atg ttt gga tagttttcg        1181
141 Pro Phe Glu Arg Trp Val Thr Ala Gln Ala Met Phe Gly
142                     335                     340
144 ggctttatc aacagccaat aacagctctt tcgcccattg aggtggaggg gctgttttt      1241
146 catgccgtaa ggaaagtgca agtaagtgaa atc                                 1274
149 <210> SEQ ID NO: 2
151 <211> LENGTH: 343
153 <212> TYPE: PRT
155 <213> ORGANISM: Corynebacterium glutamicum
159 <400> SEQUENCE: 2
161 Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn
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165 Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser
166             20                      25                      30
169 Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg
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170         35                  40                  45
173 Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg
174     50                  55                  60
177 Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys
178 65                  70                  75                  80
181 Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp
182                 85                  90                  95
185 Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp
186             100                 105                 110
189 Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp
190         115                 120                 125
193 Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val
194     130                 135                 140
197 Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser
198 145                 150                 155                 160
201 His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp
202             165                 170                 175
205 Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile
206             180                 185                 190
209 Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg
210         195                 200                 205
213 Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly
214     210                 215                 220
217 Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp
218 225                 230                 235                 240
221 Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp
222             245                 250                 255
225 Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly
226             260                 265                 270
229 His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala
230         275                 280                 285
233 Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe
234     290                 295                 300
237 Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe
238 305                 310                 315                 320
241 Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val
242             325                 330                 335
245 Thr Ala Gln Ala Met Phe Gly
246             340
249 <210> SEQ ID NO: 3
251 <211> LENGTH: 20
253 <212> TYPE: DNA
255 <213> ORGANISM: PCR primer
259 <400> SEQUENCE: 3
260 aactgcagct ctggcgatta                                      20
263 <210> SEQ ID NO: 4
265 <211> LENGTH: 20
267 <212> TYPE: DNA
269 <213> ORGANISM: PCR primer
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273 <400> SEQUENCE: 4
274 aactatccaa acattgcctg   20

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